

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 4, 2002, 01:54:20 ; Search time 52.3933 Seconds
(without alignments)
1592.744 Million cell updates/sec

Title: US-09-805-550-2

Perfect score: 2036
Sequence: 1 MRLNVKTLKGTNFEIASP.....EELTANYLLDHGHEPDDQQ 405

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP rhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriophage:*
17: SP archaea:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1211.5	59.5	389	10	Q9STA6	Q9sta6 lycopersico
2	1199.5	58.9	378	10	Q9PFI6	Q9pfi6 arabidopsis
3	1198.5	58.9	378	10	Q9AC35	Q9ac35 arabidopsis
4	1188.5	58.4	419	10	Q9M887	Q9m887 arabidopsis
5	1187.5	58.3	382	10	Q03990	Q03990 daucus caro
6	1127	55.4	392	10	Q40742	Q40742 oryza sativ
7	944.5	46.4	365	10	Q9ACE9	Q9ace9 arabidopsis
8	925.5	45.5	379	10	Q03991	Q03991 daucus caro
9	840.5	41.3	367	10	Q9MA10	Q9ma10 arabidopsis
10	832	31.0	409	4	Q8WDB0	Q8wdb0 homo sapien
11	533	26.7	246	10	Q9S9L8	Q9s9l8 arabidopsis
12	501	24.6	341	5	Q97135	Q97135 dictyostell
13	481	23.6	414	5	Q9V3W9	Q9v3w9 drosophila
14	478	23.5	414	5	Q9XEO0	Q9xeo0 drosophila
15	436.5	21.4	372	5	Q23451	Q23451 caenorhabdi
16	376.5	18.5	748	6	F79370	F79370 oryctolagus

17	361.5	17.8	113	10	Q9SA20	Q9sa20 arabidopsis
18	317	15.6	290	5	Q9VCD5	Q9vcd5 drosophila
19	271	13.3	65	10	Q9SCA8	Q9sca8 lycopersico
20	243	11.9	575	10	Q9FWF5	Q9fwf5 oryza sativ
21	231.5	11.4	551	10	Q9AC51	Q9ac51 arabidopsis
22	229.5	11.3	551	10	Q9S1I8	Q9s1i8 arabidopsis
23	222	10.9	582	11	Q9JUP9	Q9jup9 ratu
24	214.5	10.5	523	5	Q9NIF3	Q9nif3 dictyostell
25	213	10.5	582	11	Q8R317	Q8r317 mus musculu
26	210	10.3	538	10	Q9S1I9	Q9s1i9 mus musculu
27	210	10.3	595	6	Q9SME9	Q9sm9 bos tauru
28	209	10.3	582	11	Q9QZM1	Q9qzm1 mus musculu
29	202.5	9.9	502	5	Q18672	Q18672 caenorhabdi
30	197.5	9.7	596	11	Q9YNB8	Q9ynb8 mus musculu
31	197	9.7	589	4	Q9UMX0	Q9umx0 mus musculu
32	196	9.6	601	4	Q9NRR5	Q9nrr5 homo sapien
33	193	9.5	142	10	Q9LEP9	Q9lep9 homo sapien
34	193	9.5	589	4	Q9H0T8	Q9h0t8 homo sapien
35	184.5	9.1	638	11	Q9QZM0	Q9qzm0 mus musculu
36	180	8.8	589	4	Q9H3R4	Q9h3r4 homo sapien
37	179.5	8.8	101	5	Q9GZJ7	Q9gzj7 hydractinia
38	166.5	8.2	624	4	Q9UHD9	Q9uh9 homo sapien
39	166.5	8.2	624	4	Q9HAZ4	Q9haz4 homo sapien
40	164.5	8.1	1022	5	Q96073	Q96073 drosophila
41	159.5	7.8	1931	10	Q8W2U3	Q8w2u3 oryza sativ
42	158	7.8	545	5	Q9TX05	Q9tx05 caenorhabdi
43	157.5	7.7	314	4	Q9H8R7	Q9h8r7 homo sapien
44	157.5	7.7	585	13	Q9PVN8	Q9pvn8 xenopus lae
45	157	7.7	1527	3	Q8WZ15	Q8wz15 yarrowia li

ALIGNMENTS

RESULT 1

Q9STA6 PRELIMINARY; PRT; 389 AA.
ID Q9STA6
AC Q9STA6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE RAD23 protein.
GN RAD23.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=CV. WEST VIRGINIA 106; TISSUE=FRUIT;
RA Lemaire-Chamley M., Petit J., Raymond P., Chevalier C.,
RT "Analysis of gene expression during early tomato fruit development by
RT mRNA differential display."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ243875; CAB51544.1; -
DR HSSP: P54725; IDV0.
DR InterPro: IPR004806; Rad23.
DR InterPro: IPR000449; UBA_domain.
DR InterPro: IPR000626; Ubiquitin.
DR Pfam: PF00627; UBA; 2.
DR Pfam: PF00240; ubiquitin; 1.
DR SMART: SM00165; UBA; 2.
DR SMART: SM00213; UBO; 1.
DR TIGRPFAMs: TIGR00601; rad23; 1.
DR PROSITE: PS50053; UBIDITIN_2; 1.
SQ SEQUENCE 389 AA; 41508 MW; D2BAEDFOFE70778A CRC64;

Query Match 59.5%; Score 1211.5; DB 10; Length 389;
Best Local Similarity 63.0%; Pred. No. 14e-65;
Matches 255; Conservative 43; Mismatches 88; Indels 19; Gaps 6;
Qy 1 MRLNVKTLKGTNFEIASPDAVSADVKKRIETGQSTYRADQMLYQGIKLDETTL 60

```

DB 1 MKLEVTTLGTHFEIEVKEDSVADYKKNIESVQGDVYPAQOMLTHOGKVLKDTTLE 60
OY 61 SNGVAENSEFLVIMLSKRAKSSGASATATAKAPATLAQAPAPVAPASVARTPTQ 117
DB 61 ENKVAENSEFLVIMLSKRAKSSGASATATAKAPATLAQAPAPVAPASVARTPTQ 118
OY 118 VATAETAPPSVQQAAPATVATDADYVSOASNLVFGNNIEQITQOILDMGGTWER 177
DB 119 QSASESAP---TPAPVPAASST---DYDDAASNLVAGSNLETTVOOILDMGGGSMR 172
OY 178 DTVVRLRAAYNNPERAIDYLSGIPENVEAOPVAPAAQGTQNOAASPAQPAVALPV 237
DB 173 DTVVRLRAAYNNPERAIDYLSGIPENVEAOPVAPAAQGTQNOAASPAQPAVALPV 232
OY 238 QSPASAPGAPNAPLPLFPQGVPSGSGNPGVPSGSGALDALRQLPQFALLQVQANQ 297
DB 233 QLAVPSSGPNAPLPLFPQGLTFMAGSN-----AGAGNIDFLRNSQFQALRAMVQANQ 286
OY 298 ILOPMLQELGKONPOLRLIOENQAEFLVLVNESPEGPGGNILGQLAANVQTLVTPE 357
DB 287 ILOPMLQELGKONPOLRLIOENQAEFLVLVNESPEGPGGNILGQLAANVQTLVTPE 344
OY 358 EREARLORLEGMGFRELVEVFPACNKBDELANTYLLDHGHEFD 402
DB 345 EREARLORLEGMGFRELVEVFPACNKBDELANTYLLDHGHEFD 389

RESULT 2
O9F16 PRELIMINARY: PRT: 378 AA.
AC 09F16:
DB 01-MAR-2001 (TREMBLrel. 16, Created)
DB 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DB 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DB DNA repair protein RAD23 homolog (Hypothetical 40.1 kDa protein)
DE (At5g38470/At5g38470).
DE Arabidopsis thaliana (Mouse-ear cress).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_Taxid=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=97471569; PubMed=9330910;
RA Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,
RA Miyajima N., Tabata S.:
RT "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence
RT features of the 1.6 Mb regions covered by twenty physically assigned
RT pl clones."
RL DNA Res. 4:215-230(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Koeseema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Onda C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Tortum M., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.:
RT "Arabidopsis cDNA clones."
RT Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Meyers M.C., Shinn P., Banh J.,
RA Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Onda C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Tortum M., Wu H.C., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,

```

```

RA Ecker J.R.:
RT "Arabidopsis ORF clones."
RL Submitted (Mar-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB005248; BAB09359.1; -
DR EMBL: AY058196; BAL25609.1; -
DR EMBL: AY081835; AAL87405.1; -
DR HSP: P54725; IDVO.
DR Interpro: IPR004806; Rad23.
DR Interpro: IPR000449; UBA_domain.
DR Interpro: IPR000626; Ubiquitin.
DR Pfam: PF00627; UBA_2.
DR Pfam: PF00240; ubiquitin; 1.
DR SMART: SM00165; UBA_2.
DR SMART: SM00213; UBQ; 1.
DR TIGRFAMs: TIGR00601; rad23; 1.
DR PROSITE: PS0053; UBIQUITIN_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 378 AA; 40066 MW; DD9B59135EA366A9 CRC64;

Query Match 58.9%; Score 1199.5; DB 10; Length 378;
Best Local Similarity 62.9%; Pred. No. 7; 1e-65;
Matches 256; Conservative 43; Mismatches 75; Indels 33; Gaps 9;

OY 1 MKLVNKTGTFEIEASPDASVADYKRIETTGQGSTYRADQMLTQKILKDTTLE 60
DB 1 MKLVNKTGTFEIEVKEDSVADYKKNIESVQGDVYPAQOMLTHOGKVLKDTTLE 59
OY 61 SNGVAENSEFLVIMLSKRAKSSGASATATAKAPATLAQAPAPVAPASVARTPTQ 116
DB 60 ENKVAENSEFLVIMLSKRAKSSGASATATAKAPATLAQAPAPVAPASVARTPTQ 111
OY 117 PVATETAPPSVQQAAPATVATDADYVSOASNLVFGNNIEQITQOILDMGGTWER 176
DB 112 PVPSTGA-----TAAAP--TAAVQTDVYGGAAASNLVAGTTLESTVOOILDMGGGSMW 164
OY 177 RDTVVRLRAAYNNPERAIDYLSGIPENVEAOPVAPAAQGTQNOAASPAQPAVALPV 236
DB 165 RDTVVRLRAAYNNPERAIDYLSGIPENVEAOPVAPAAQGTQNOAASPAQPAVALPV 221
OY 237 VOPSPASAPGAPNAPLPLFPQGVPSGSGNPGVPSGSGALDALRQLPQFALLQVQANP 296
DB 222 --PAATGCGPNAPLPLFPQGVPSGSGNPGVPSGSGALDALRQLPQFALLQVQANP 273
OY 297 QILOPMLQELGKONPOLRLIOENQAEFLVLVNESPEGPGGNILGQLAANVQTLVTPT 356
DB 274 QILOPMLQELGKONPOLRLIOENQAEFLVLVNESPEGPGGNILGQLAANVQTLVTPT 331
OY 357 EREARLORLEGMGFRELVEVFPACNKBDELANTYLLDHGHEFDQ 403
DB 332 EREARLORLEGMGFRELVEVFPACNKBDELANTYLLDHGHEFDQ 378

RESULT 3
O94C35 PRELIMINARY: PRT: 378 AA.
AC 094C35:
DB 01-DEC-2001 (TREMBLrel. 19, Created)
DB 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DB 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 40.1 kDa protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_Taxid=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Koeseema E., Meyers M.C., Shinn P.,
RA Bowser L., Carninci P., Bowser L., Carninci P., Chung M.K.,
RA Tracy S.E., Banh J., Bowser L., Carninci P., Jones T., Kamiya A.,
RA Goldsmith A.D., Hayashizaki Y., Ishida J., Jones T., Kamiya A.,
RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Pham P.K., Quach H.L.,
RA Sakano H., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C.,

```

RA Toriumi M., Yamada K., Yu G., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis cDNA clones.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY037181; AAK59766.1; -
DR InterPro: IPR004806; Rad23.
DR InterPro: IPR000449; UBA_domain.
DR InterPro: IPR000626; Ubiquitin.
DR Pfam: PF00627; UBA; 2.
DR TIGRPFAM: TIGR00601; rad23; 1.
DR PROSITE: PSS0053; UBIQUITIN_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 378 AA; 40075 MW; E49B591527A3EC27 CRC64;

Query Match 58.9%; Score 1198.5; DB 10; Length 378;
Best Local Similarity 62.9%; Pred. No. 8.2e-65;
Matches 256; Conservative 43; Mismatches 75; Indels 33; Gaps 9;

QY 1 MKLNKTLKGTNEFIENSPDASVADYKRIETTGOSTYRADOQMLYQGIKIDETTL 60
DB 1 MKLFVKTLSGNEFEIKPKADKVSVDYKTAIEFVKG-AEYPAKQMLIHQKVLKDETTLE 59
QY 61 SNGVAENSFLVIMLSKAKASSGASTAT-TAKAPATIAQAPAPAPAPASVARTTQA 116
DB 60 ENNVENSEFTVIMLSKTKASPSGASTASADAPAPATQPTATPQVS-APYASV----- 111
QY 117 PVATAETAPSPVQPAAPATVAATDDADYVSOAASNLVFGNNLEQTIQOILDMGSGTWE 176
DB 112 PVTTSIGA-----TAAAPA--TAASVOTDYGAASNLVAGTILESTVQOILDMGSGSWD 164
QY 177 RDTVVRALRAAYNNPERAIDYLSGIPENVEAOPVAPAPAGQOTNOAASPAQPAVALP 236
DB 165 RDTVVRALRAAFNNPERAIVLYLSGIPAPQAEIPVAPQAPATGEQANPLAQPOQAAA--- 221
QY 237 VQSPASAGNANPLNFPQGVPSGSGNPGVVGAGSGALDALROLPOFQALLQVQANP 296
DB 222 --PAAATGGNANPLNFPQGMPPADA-----GAGAGNLDLFKNSHOFALRLAMVQANP 273
QY 297 QIILQPMLOELGKONPOLILRIQENQAEFLRLVNESPEGPGCNILGOLAAVPTLTVT 356
DB 274 QIILQPMLOELGKONPOLIVRLIOHQADFRLINPEVGE--ANMEDLEAAMPQAVYVTP 331
QY 357 EEBEATIQLEGMGFNRELVEVEFACNKEDELTANYLLDHGHEFDDQ 403
DB 332 EEBEATIRELGMGFDRAMVLEVEFACNKEBELANYLLDHMHHEFDDQ 378

RESULT 4
Q9M887 PRELIMINARY; PRT; 419 AA.
AC Q9M887;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Putative RAD23 (At3g902540/F16B3_17).
GN F16B3.17.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosidae;
OC eudicots II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
ON (1)
RN SEQUENCE FROM N.A.
RP STRAIN=CV, COLUMBIA;
RC Lin X., Kaul S., Town C.D., Beato M., Creasy T.H., Haas B., Wu D.,
RA Rouning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
RA Bowman C.L., White O., Niernan W.C., Fraser C.M.;
RT "Arabidopsis thaliana chromosome III BAC F16B3 genomic sequence.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN 12)
RP SEQUENCE FROM N.A.
RA Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,

RA Bowser L., Carinici P., Dale J.M., Gibson H.A., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,
RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
RA Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Yamada K., Yu G., Yu S., Shinozaki K.,
RA Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis cDNA clones.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC021640; AAF32461.1; -
DR EMBL: AY039562; AAK62617.1; -
DR HSSP: P54725; IDV0.
DR InterPro: IPR002965; P-rich_extensn.
DR InterPro: IPR004806; Rad23.
DR InterPro: IPR000449; UBA_domain.
DR InterPro: IPR000626; Ubiquitin.
DR Pfam: PF00627; UBA; 2.
DR Pfam: PF00240; ubiquitin; 1.
DR PRINTS: PRO1217; PRICHEXTENS.
DR SMART: SM00165; UBA; 2.
DR SMART: SM00213; UBQ; 1.
DR TIGRPFAM: TIGR00601; rad23; 1.
DR PROSITE: PSS0053; UBIQUITIN_2; 1.
SQ SEQUENCE 419 AA; 44247 MW; CAA13BC4FFB1E25 CRC64;

Query Match 58.4%; Score 1188.5; DB 10; Length 419;
Best Local Similarity 58.4%; Pred. No. 3.7e-64;
Matches 253; Conservative 53; Mismatches 82; Indels 45; Gaps 10;

QY 1 MKLNKTLKGTNEFIENSPDASVADYKRIETTGOSTYRADOQMLYQGIKIDETTL 60
DB 1 MKLFVKTLSGNEFEIKPKADKVSVDYKRIETTSVQADYVPAKQMLIHQKVLKDETTIE 60
QY 61 SNGVAENSFLVIMLSKAKASSGASTAT-TAKA-----PATIAQAPAPAP 105
DB 61 ENKVAENSFLVIMKNSKAPSAASASAGTSQAKSTPSTQPSISPTQIPASVAP 120
QY 106 AAS-----VARTPTQAPVATETAPPVQAPAPATVAAT-----DDADYVSOAAS 152
DB 121 APTRPPPPAPTPPAPVAPAAETVTPPI-PEVPATISSPTAPDASVSGDVGQAAS 179
QY 153 NLVFGNNLEQTIQOILDMGSGTREDVVRALRAAYNNPERAIDYLSGIPENVEAOPVA 212
DB 180 NLAAGSNLESTIQOILDMGGTMDRETVALRAAFNNPERAIVLYTGTPEQAEVPVA 239
QY 213 RAPAGQOTNOAASPAQPAVALPVPQSPASAGNANPLNFPQGVPSGSGNPGVVGAG 272
DB 240 RPPASAGOPANPPAQTOQPAHA-----PAS-GPNANPLDLPQGLPVGGNP-----G 286
QY 273 SGALDALROLPOFQALLQVQANPOLIOLPMLOELGKONPOLILRIQENQAEFLRLVNESP 332
DB 287 AGTLDLFKNSQGFQALRAMVQANPOLVLPMLQELGKONPNLMRLIOHQADFRLINPEV 346
QY 333 E-GPGGNIIGQLAAAY--PQTLTVPEBEAIDIRLGMGFNRELVEVEFACNKEDELT 389
DB 347 EGGESENLLGQMAAGPQOALQIVTHEBEAIRELBEAMGERALVLEVEFACNKEDELA 406
QY 390 ANYLLDHGHEFDD 402
DB 407 ANYLLDHHEFEE 419

RESULT 5
O03990 PRELIMINARY; PRT; 382 AA.
ID O03990;
AC O03990;
DT 01-JUL-1997 (TREMblrel. 04, Created)
DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE RAD23, Isoform I.
OS Daucus carota (Carrot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae: euasterids II; Apiales; Apiaceae; Daucus.
 OX NCBI_TaxID=4039;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN=WM001C
 RX MEDLINE=98345597; PubMed=9681019;
 RA Sturm A., Leinhard S.;
 RT "Two isoforms of plant RAD23 complement a UV-sensitive rad23 mutant in yeast.";
 RT Plant J. 13:815-821(1998).
 DR EMBL: Y12013; CAZ72741.1; -
 DR HSSP: p54725; IDV0.
 DR InterPro: IPR004806; Rad23.
 DR InterPro: IPR000449; UBA_domain.
 DR InterPro: IPR000626; Ubiquitin.
 DR Pfam: PF00627; UBA; 2.
 DR Pfam: PF00240; ubiquitin; 1.
 DR SMART: SM00165; UBA; 2.
 DR SMART: SM00213; UBA; 1.
 DR TIGRfams: TIGR00601; rad23; 1.
 DR PROSITE: PS50053; UBQUITIN_2; 1.
 DR PROSITE: PS50053; UBQUITIN_2; 1.
 SQ SEQUENCE 382 AA; 40344 MW; 27EF02A2402F3DC2 CRC64;

Query Match 58.3%; Score 1187.5; DB 10; Length 382;
 Best Local Similarity 62.7%; Pred. No. 3.8e-64;
 Matches 253; Conservative 46; Mismatches 75; Indels 31; Gaps 11;

OY 1 MLNVTTLKGTNFEIEASPDASADVARIETGOSTYRADQOMLIYOGKILKDETTLE 60
 DB 1 MIIYVTKLGSFIEQVNDSDVADYKRIETGOGHITPAQOMLIYOGKILKDETTLL 60
 OY 61 SNGVAENSEFLVIMLSKAKASSSGASTATTAT---KAPATLAQPAAPVAPASVARTPTQAP 117
 DB 61 ENNVAVENSEFLVIMLSKSKSPSGESTTTPAAAPKAPOTSAPSPVP-APAVS-----QPP 113
 OY 118 VTAET-AP-PSVQQAAPATAATDADYVSOAASNTVFGNNLEQTTOOILDMGGW 175
 DB 114 ASTLVPAVSPAPATATATPSAAVSEANVDSASTLVASNLGALIOQLIDMGGWTW 173
 OY 176 ENDTVRALRAAYNNPRAIDYLSGIPENVEAOPVARAPAGQOTNOOASPA-OPAVA 234
 DB 174 DEDTVIRIYRAFNPERAVERLYSGIPQAEPAPVAPSPSG-----QANPDLQPPAPA 228
 OY 235 LPVQSPASAGNANPLNLFPGVPSGGSNPGVPGAGSALDALROLPOFALLQVLA 294
 DB 235 -AQPAPASAGNANPLNLFPGVPSGGSNPGVPGAGSALDALROLPOFALLQVLA 281
 OY 295 NFOIIPMLQELGKONPOLRLIOENQAEFLRLVNESPEGSGGNTIGOLAAVPOTLV 354
 DB 287 NFOIIPMLQELGKONPOLRLIOENQAEFLRLVNESPEGSGGNTIGOLAAVPOTLV 335
 OY 355 TPBERAIORELGNGFNRELVEVFACNKDELTANYLLDHGHEPD 401
 DB 336 TPBERAIORELGNGFNRELVEVFACNKDELTANYLLDHGHEPD 382

RESULT 6
 Q40742 PRELIMINARY; PRT; 392 AA.

AC Q40742;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE OSRAD23.
 OS Oryza sativa (Rice).
 OC Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Euphorbiaceae; Oryzaeae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=NIPONBARE;
 RX MEDLINE=97369378; PubMed=9225866;

RA Schultz T.F., Qualtrano R.S.;
 RT "Characterization and expression of a rice RAD23 gene.";
 RL Plant Mol. Biol. 34:557-562(1997).
 DR EMBL: U63530; AAB65841.1; -
 DR HSSP: p54725; IDV0.
 DR InterPro: IPR004806; Rad23.
 DR InterPro: IPR000449; UBA_domain.
 DR InterPro: IPR000626; Ubiquitin.
 DR Pfam: PF00627; UBA; 2.
 DR Pfam: PF00240; ubiquitin; 1.
 DR SMART: SM00165; UBA; 2.
 DR SMART: SM00213; UBA; 1.
 DR TIGRfams: TIGR00601; rad23; 1.
 DR PROSITE: PS50053; UBQUITIN_2; 1.
 DR PROSITE: PS50053; UBQUITIN_2; 1.
 SQ SEQUENCE 392 AA; 41754 MW; BD6E0B574CCTCAB CRC64;

Query Match 55.4%; Score 1127; DB 10; Length 392;
 Best Local Similarity 59.1%; Pred. No. 1.8e-60;
 Matches 243; Conservative 48; Mismatches 90; Indels 30; Gaps 9;

OY 1 MLNVTTLKGTNFEIEASPDASADVARIETGOSTYRADQOMLIYOGKILKDETTLE 60
 DB 1 MIIYVTKLGSFIEQVNDSDVADYKRIETGOGHITPAQOMLIYOGKILKDETTLL 60
 OY 61 SNGVAENSEFLVIMLSKAKASSSGASTATTAT---KAPATLAQPAAPVAPASVARTPTQAP 118
 DB 61 ENNVAVENSEFLVIMLSKSKSPSGESTTTPAAAPKAPOTSAPSPVP-APAVS-----QPP 111
 OY 119 ATAETP-----PSVQQAAPATAATDADYVSOAASNTVFGNNLEQTTOOILDMGG 173
 DB 112 APRTVPTVSAFTPATATSPAPAVASSEADYGGATSNLVAAGSLNLTGOSTILEMGG 171
 OY 174 TWEDTVRALRAAYNNPRAIDYLSGIPENVEAOPVARAPAGQOTN-OOAASPAQA 232
 DB 172 IMDROIVLALSAFNPRRAVERLYSGVPEQMDI-PV--PPPSIQAPAPPTQASQATQA 228
 OY 233 VALPVPSPASAGNANPLNLFPGVPSGGSNPGVPGAGSALDALROLPOFALLQVLA 292
 DB 229 A-----PSILSSGPNASPLDLEFPALPNASTD-----AAGLGNLALRNNAOFRLLSLV 278
 OY 293 QANPOLIOMLELGKONPOLRLIOENQAEFLRLVNESPEGSGGNTIGOLAAVPOTLV 352
 DB 279 QANPOLIOMLELGKONPOLRLIOENQAEFLRLVNESPEGSGGNTIGOLAAVPOTLV 338
 OY 353 TPBERAIORELGNGFNRELVEVFACNKDELTANYLLDHGHEPD 403
 DB 339 AVTPBERAIORELGNGFNRELVEVFACNKDELTANYLLDHGHEPD 389

RESULT 7
 Q94CE9 PRELIMINARY; PRT; 365 AA.

AC Q94CE9;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Putative RAD23 protein.
 DE F20B17.8.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RN SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
 RA Goldsmith A.D., Lee J.M., Quach H.L., Tang C., Totlum M., Yu G.,
 RA Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J.,
 RA Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koeseema E.,
 RA Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M.,
 RA Palm C.J., Sakurai T., Satou M., Seki M., Shim P., Southwick A.,
 RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.,
 RA "Full Length cDNA of gene F20B17.8 (GI:7715605).";

RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,
RA Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C.,
RA Yamamura Y., Yu G., Yu S., Bowser L., Carinetti P., Chen H., Cheuk R.,
RA Hayashitaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Kim C., Koeseke E., Lam B., Lin J., Meyers M.C., Miranda M.,
RA Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,
RA Shinn P., Southwick A., Shinzaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Full length cDNA of gene F20B17.8 (GI:77155605).";
RT Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY034912; AAK59419.1; -;
DR EMBL; AY063103; AAL34277.1; -;
DR InterPro: IPR004806; Rad23.
DR InterPro: IPR000449; UBA.domain.
DR InterPro: IPR000626; Ubiquitin.
DR Pfam; PF00627; UBA; 2.
DR Pfam; PF00240; ubiquitin; 1.
DR TIGRFAMs; TIGR00601; rad23; 1.
DR PROSITE; PS50053; UBQUITIN_2; 1.
SQ SEQUENCE 365 AA; 39157 MW; 4FED9EC59B467745 CRC64;

Query Match 46.4%; Score 944.5; DB 10; Length 365;
Best Local Similarity 50.5%; Pred. No. 1.7e-49;
Matches 206; Conservative 56; Mismatches 97; Indels 49; Gaps 9;

QY 1 MKNLVTKLGTNEIEASPDASVADYKRITETGOGSTYRADQMLYQKILKDETTLE 60
DB 1 MKNLVTKLGTNEIEASPDASVADYKRITETGOGSTYRADQMLYQKILKDETTLE 60
QY 61 SNGVAENSEFLYIMLSKAKA-SSSGASTATTAKAPATLAQPAAPVAPASVARTPTQAPVA 119
DB 61 ENKVTGEGLVYMLGKSKSGSAGASVQPVSAFTTSSTKRAAP-----STTQSPV 111
QY 120 TATTAAPSVOQAAPATVAATDADYVQAASNLVFGNNLEQRTIQOILDMGGTWERDT 179
DB 112 PAPTAPQEDPAA-----QTPDYGAASLTIVSGSSLEQWVQOIMEMGGGSMKET 161
QY 180 VVALRAAYNNPERAIDYLSGIPENVE-AQVAPARAQAQRTNQQAASAPAPVALPVQ 238
DB 162 VTVALRAAYNNPERAIDYLSGIPQRAEAVVPVPEAQIAG-----SGAAPV- 207
QY 239 PSPASGPNANPLNLFPGVPSGSGSNPGVPGAGS--GALDALRQLPQFQALQLQVQAN 295
DB 208 -APASGSPNSPLDLPQ-----ETVAAAGSGDLGLEFLERNNDDQQLRTMHSN 257
QY 296 POLQPMQLGKQNPQILRLIOENQAEFLVNESPEGGPG-GNIIQLAALAVPQTLTV 354
DB 258 POLQPMQLGKQNPQILRLIOENQAEFLQVNEPEYEGSDGEGDMQDPEQEMPHAINV 317
QY 355 TPPEERAIORLEGKGFRELVLEVFACNKEDELTANTLLDHGHEFDD 402
DB 318 TPPEERAIORLEGKGFRELVLEVFACNKEDELTANTLLDHGHEFDD 365

RESULT 8
003991 PRELIMINARY; PRT; 379 AA.
AC 003991;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE RAD23 protein, isoform II.
OS Daucus carota (Carrot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; eusterids II; Apiales; Apiales; Daucus.
OX NCB1_TaxID=4039;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M001C;

RX MEDLINE=98345997; PubMed=9681019;
RA Sturm A., Leinhard S.;
RT "Two isoforms of plant RAD23 complement a UV-sensitive rad23 mutant in
RT yeast.";
RL Plant J. 13:815-821(1998).
DR EMBL; Y12014; CAA72742.1; -;
DR HSSP; P54725; IDV0.
DR InterPro: IPR004806; Rad23.
DR InterPro: IPR000449; UBA.domain.
DR InterPro: IPR000626; Ubiquitin.
DR Pfam; PF00627; UBA; 2.
DR Pfam; PF00240; ubiquitin; 1.
DR SMART; SM00165; UBA; 2.
DR TIGRFAMs; TIGR00601; rad23; 1.
DR PROSITE; PS50053; UBQUITIN_2; 1.
SQ SEQUENCE 379 AA; 40530 MW; B26697BA39CC5929 CRC64;

Query Match 45.5%; Score 925.5; DB 10; Length 379;
Best Local Similarity 50.2%; Pred. No. 2.4e-48;
Matches 203; Conservative 57; Mismatches 117; Indels 27; Gaps 8;

QY 1 MKNLVTKLGTNEIEASPDASVADYKRITETGOGSTYRADQMLYQKILKDETTLE 60
DB 1 MKNLVTKLGTNEIEASPDASVADYKRITETGOGSTYRADQMLYQKILKDETTLE 60
QY 61 SNGVAENSEFLYIMLSKAKA-SSSGASTATTAKAPATLAQPAAPVAPASVARTPTQAPVA 119
DB 61 ESKISEDEGLVYMLGKSKTMSSTGTTPAQAQSSAPAPPAAPVAPAPAPAPASAVIPNT 120
QY 120 TATTAAPSVOQAAPATVAATDADYVQAASNLVFGNNLEQRTIQOILDMGGTWERDT 179
DB 121 TVPAP--LSPAPAP-----SDTYGEAASNVVAGSNLEQRTIQHMDGGGMMPTNM 169
QY 180 VVALRAAYNNPERAIDYLSGIPENVEAQ-PVAPARAQAQRTNQQAASAPAPVALPVQ 238
DB 170 VVALRAAYNNPERAIDYLSGIPENVEAQAAPVASH--FQGOIAGNNAALSDNGVA---- 223
QY 239 PSPASGPNANPLNLFPGVPSGSGSNPGVPGAGS--GALDALRQLPQFQALQLQVQAN 298
DB 224 -GAAPGAPNSPLNMFQETISG-----VTGAGLGSLEFLRNRPQOTRLSMVQRNPQI 276
QY 299 LQPMQLGKQNPQILRLIOENQAEFLVNESPEGGPGNIIQLAALAVPQTLTVPEE 358
DB 277 LQPMQLGKQNPQILRLIOENQAEFLQVNEPEYEGSDGEGDMQDPEQEMPHAINV 335
QY 359 REAIORLEGKGFRELVLEVFACNKEDELTANTLLDHGHEFDD 402
DB 336 REAIORLEGKGFRELVLEVFACNKEDELTANTLLDHGHEFDD 379

RESULT 9
09MA10 PRELIMINARY; PRT; 367 AA.
AC 09MA10;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE F20B17.8.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OX eurosids II; Brassicales; Brassicaceae; Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.
RA Khan S., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Kim C.,
RA Shinn P., Altati H., Bel Q., Chin C., Chlou J., Choi E., Conn L.,
RA Conway A., Gonzales A., Hansen N., Howey B., Koo T., Lam B., Lee J.,
RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharasy N., Nguyen M.,
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thavert A.,
RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA Ecker J.R.;

*Genomic sequence for Arabidopsis thaliana BAC F20B17 from chromosome
RT 1.
RT Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Ecker J.R.
RA Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Ecker J.R.
RA Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
RA Khan S., Kim C., Altafi H., Bel B., Chin C., Chlou J., Choi E.,
RA Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thavert A., Tortum M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA Theologis A., Ecker J.
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC010793; AAF68123.1; -
DR HSSP; P54725; IDV0.
DR InterPro; IPR004806; Rad23.
DR InterPro; IPR000449; UBA_domain.
DR Pfam; PF00627; UBA; 2.
DR SMART; PF00240; ubi_qultin; 1.
DR SMART; SM00213; UBO; 2.
DR TIGRFAMs; TIGR00601; rad23; 1.
DR PROSITE; PS50053; UBIQUITIN_2; 1.
SQ SEQUENCE 367 AA; 39790 MW; C6D01134B5C69CE6 CRC64;

Query Match 41.3%; Score 840.5; DB 10; Length 367;
Best Local Similarity 47.4%; Pred. No. 3.1e-43;
Matches 192; Conservative 53; Mismatches 119; Indels 41; Gaps 8;

QY 1 MKLVNLTGKTFEIASPDASVADVAKRIETTGQSTYRADQOMLYOGKILKDETTLE 60
DB 1 MKLVNLTGKSHFEIRVLPDSPTIMAVKKNIEDSGKDNPCGGQQLIHNGKYLKDETSLV 60
QY 61 SNGVENSEFLVIMLSKAKSSSGASTATYAKAPATLAQRAAPAPAPASVAKPTQAPVAT 120
DB 61 ENKVEEGFLVWLSKSKSGS---AGQASVOCVRLLFHSLFPLRLSLSTIYVPFT 116
QY 121 AETAPSVOPQAPATVATDADVYSQASNLVGNMLEQTIOILDMGGTWERDVTY 180
DB 117 CCGFTYS-----CRRITGTDITYGQAASITVSGSLEQWVQIMEMGGSDMKETV 166
QY 181 VVALRAAVNPERAIDLYSGIPEVNE-AQPVARAPAGQQTNOQASPAQPAVALVPQ 239
DB 167 TVALRAAVNPERAIDLYSGIPEVNE-AQPVARAPAGQQTNOQASPAQPAVALVPQ 211
QY 240 SPASAGPNANPLTFQGVPSGSGSNQVYPGAGSGALDLRLQ-POFQALLQVQANPQI 298
DB 212 APASGPNNSPLDLEPO-----ETVAAAGSGDLGLELRNNDQVAIITISAFSLN 262
QY 299 LQPMLOELGKQNPQILRLIQENQAEFLRLVNESPEGGPG-GNIGLQLAAPVQTLVTE 357
DB 263 CEPMLQELGKQNPQILRLIQENQAEFLRLVNESPEGGPG-GNIGLQLAAPVQTLVTE 322
QY 358 EBEAIORELEGMPNRELVEVFACNKKDELTANYLLDGHGFDD 402
DB 323 EBEAIORELEGMPNRELVEVFACNKKDELTANYLLDGHGFDD 367

RESULT 10
Q8WUB0 PRELIMINARY; PRT; 409 AA.
AC Q8WUB0;
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)

DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE RAD23 homolog B (S. cerevisiae).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=UTERUS;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020973; AAH20973.1; -
DR InterPro; IPR004806; Rad23.
DR InterPro; IPR000449; UBA_domain.
DR InterPro; IPR000626; ubi_qultin.
DR Pfam; PF00627; UBA; 2.
DR SMART; PF00240; ubi_qultin; 1.
DR SMART; SM00165; UBA; 2.
DR SMART; SM00213; UBO; 1.
DR TIGRFAMs; TIGR00601; rad23; 1.
DR PROSITE; PS50053; UBIQUITIN_2; 1.
SQ SEQUENCE 409 AA; 43199 MW; 475FBD499DACAC69 CRC64;

Query Match 31.0%; Score 632; DB 4; Length 409;
Best Local Similarity 34.5%; Pred. No. 1.3e-30;
Matches 153; Conservative 81; Mismatches 133; Indels 76; Gaps 12;

QY 1 MKLVNLTGKTFEIASPDASVADVAKRIETTGQSTYRADQOMLYOGKILKDETTLE 60
DB 1 MOYTLTKLQOQTFKIDIDDEETVKAKEIKESKGDAPVAGQIKTLINDTALK 60
QY 61 SNGVENSEFLVIMLSKAKSSSGASTATYAKAPATLAQRAAPAPAPASVAKPTQAPVAT 109
DB 61 EKKIDENFVVMVTKPKAVSTPAPATQGSAPASTTAVSTTTTVAQAPTPV-PALAP 119
QY 110 ARTPTQ-----APVATETAPSVOPQAPAT-VAATDD-----ADVYSQ 149
DB 120 TSTPASITPASATASSEPAPASAKOEKPAETPAETPAETPAETPAETPAETPAETPAET 179
QY 150 AASNLVFGNNLQOTIOILDMGGTWERDVTYRALRAAVNPERAIDLYSGIPEVNEQ 209
DB 180 AITSALVTGSGYENMYTEISMG---YERQVIAALRASNNPDRVETLMKIPGDRSQ 236
QY 210 PVARAPAGQQTNOQAS---PAQPAVALVPQSPASAGPNANPLTFQGVPSGSGSNQ 266
DB 237 AYVADP-----QAASGVPOSSAVAAAATTTAT-----TTSSGGHP- 275
QY 267 VYPGAGSGALDLRLQPOQALLQVQANPQILQPMLOELGKQNPQILRLIQENQAEFLR 326
DB 276 -----LEFLRNQPOQKROIQONPSLLPALQOIGRENQOLLOISQHOEHFQ 326
QY 327 LVNE-----SPGGPGGNLQGLAAV---QTLVYTPPERAIORELEGMPNRELVEV 378
DB 327 MINEPVQENAGGGGGGGGGGGAIEAGSGHANYIOTVTPKEAIEKALGFPBGLVIOA 386
QY 379 FFACNKKDELTANYLLDGHGFDD 401
DB 387 YFACENKENVLANPFLQGNFDD 409

RESULT 11
Q9S9L8 PRELIMINARY; PRT; 246 AA.
AC Q9S9L8;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE T24D18.27 protein.
GN T24D18.27.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustoids II; Brassicales; Brassicaceae; Arabidopsids.

OX NCBI_TaxID=3702;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Liu S.X., Yu G., Sakano H., Jhaveri A., Lee J.M., Ienz C., Pham P.,
RA Tortumli M., Chin C., Chlou J., Choi E., Chung M., Gonzalez A.,
RA Huang B., Koo T., Li J., Liu A., Vaysberg M., Altali H., Brooks S.,
RA Buehler E., Chao Q., Conn L., Conway A., Hansen N., Johnson-Hopson C.,
RA Khan S., Kim C., Lam B., Nguyen M., Palm C., Shin P., Tambunga G.,
RA Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
RT "The sequence of BAC T2418 from Arabidopsis thaliana chromosome 1.";
RU Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Theologis A.;
RU Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR HSSP; P02248; UBI.
DR InterPro; IPR000449; UBA_domain.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00240; ubiquitin.1.
DR SMART; SM00165; UBA; 1.
DR SMART; SM00213; UBO; 1.
DR PROSITE; PS50053; UBIQUITIN_2; 1.
SQ SEQUENCE 246 AA; 25966 MW; 0867D1E7D72B6FEE CRC64;

Query Match 26.7%; Score 543; DB 10; Length 246;
Best Local Similarity 41.8%; Pred. No. 1.7e-25;
Matches 117; Conservative 41; Mismatches 74; Indels 48; Gaps 4;

QY 1 MKLWVKTLKGTNEIEASPDASVADVRIETTGOSTYRADQOMLYOGKILNDETTLE 60
DB 1 MKLVKTKLKGSHREIVLPDTIMAVKKNIEDSGSKDNYPCGQDLHNGKVLKDETTLY 60
QY 61 SNGVAENSFLVIMLSKAKSSGASTATTAAPATLAQAPAPAPAPASVATPPQAPVAT 120
DB 61 ENKYTEGFLVIMLSKSKTASAPSTQLAAPSTQSIIVPAPASNPVQEPAP----- 115
QY 121 AETAPPEVQOAPPAATVAATDADVYQSAASNLVFGNNLEQTQOILDMGGTWERDVT 180
DB 116 -----QSDITYGQASITVSGSSSTEQMVOQIMEMGGSGMDKETV 153
QY 181 VRALRAAYNNPERAIDLYSGIPENVEAPARAPAGQOONQOAPAPAPALVYQPS 240
DB 154 TRALRAAYNNPERAVDLYSGIPETV---TIPATNLSGVSGRFLAP----- 198
QY 241 PASAGPAPNANPLNFPQGVPSGSGNPGVYPGAGCALDALR 280
DB 199 PPSGGPNSPLDLFPQEAVIDAA-----GGDLGTLLEFLR 232

RESULT 12
ID 097135 PRELIMINARY; PRT; 341 AA.
AC 097135;
DT 01-MAY-1999 (TREMblrel. 10, Created)
DT 01-MAY-1999 (TREMblrel. 10, last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, last annotation update)
DE Repc-binding protein A.
GN RCBA.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SLB153;
RA Li G., Alexander H., Alexander S.;
RT "rcba, the Dictyostelium discoideum homolog of yeast repair gene
RAD23.";
RU Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF103870; AADI7913.1; -.

DR HSSP; P54725; IDV0.
DR InterPro; IPR004806; Rad23.
DR InterPro; IPR000449; UBA_domain.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00627; UBA; 2.
DR Pfam; PF00240; ubiquitin.1.
DR SMART; SM00165; UBA; 2.
DR SMART; SM00213; UBO; 1.
DR TIGRFAMs; TIGR00601; rad23; 1.
DR PROSITE; PS50053; UBIQUITIN_2; 1.
SQ SEQUENCE 341 AA; 37528 MW; E376B909E6E57E CRC64;

Query Match 24.6%; Score 501; DB 5; Length 341;
Best Local Similarity 31.9%; Pred. No. 8.6e-23;
Matches 136; Conservative 59; Mismatches 123; Indels 108; Gaps 15;

QY 1 MKLWVKTLKGTNEIEASPDASVADVRIETTGOSTYRADQOMLYOGKILNDETTLE 60
DB 1 MKVTIKNKKEIYEVANGDLTVALKNLISEKHNT---PSWOTLLYSGKILDEKRTLE 57
QY 61 SNGVAENSFLVIMLSKAKSSGASTATTAAPATLAQAPAPAPASV----- 109
DB 58 SYNTDGGFLKMTKKR-----EAPAT--TPASTPPLNTYSTNNHHYCR 103
QY 110 -----ARTPQAPVATTAETAPPSVOPQAPAPATVATDADVYQSAASNLVFGN 158
DB 104 PNKHXLNNTSTTPTSVPTPTNNT-PATPNPTTSPTSTSTTS--PQSSDFATGT 160
QY 159 NLEGTQOILDMGGTWERDVTYRALRAAYNNPERAIDLYSGIPENVEAPARAPAG 218
DB 161 ELETKNKITMG--FARDVLLRLRTFNNAAREALEYLVSG-----NIPAN 206
QY 219 QOTNOQASAPQAPVALVQPSAPGNANPLNFPQGVPSGSGNPGVYPGAGCALDA 278
DB 207 DPEDDEE-----MGCG-----GSDNPFEE 227
QY 279 LRQLPQFQALQVQANPQILQPMQLQELGKONPQILRTIOENQAEFLVNESEGGG 338
DB 228 LRNPHEFLRLREAIKSNISILPGILOAQYNPALVROIQENPNEFLRL--QGDGNGC 285
QY 339 NILQGLAAVYQTLVNPPEEREATORLEGM--GFRRELVEFFPCNDDELTAVYLDHG 397
DB 286 N-PGQF-----TLQVQSESEAIORLQALGMKSTVIEAFACDNKEELTASYLFETA 338
QY 398 HEFDDQ 403
DB 339 ---DDE 341

RESULT 13
ID 09V3W9 PRELIMINARY; PRT; 414 AA.
AC 09V3W9;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, last annotation update)
DE RAD23 protein.
GN RAD23 OR CG1836.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blatej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abri1 J.F., Agbayeni A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Baller R.M., Basu A., Baxendale J., Bayraktiroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borrova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleissmann W.,
RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ibeagwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Ruskern D.R., Pacled J.M.,
RA Palazzolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spler E., Spredling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye Y., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).

RP SEQUENCE FROM N.A.
RA Brodsky M.H., Rubin G.M., Tsang G.;
RT "Full Length *Drosophila melanogaster* cDNA sequence.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AE003844; AAF59352.1; -;
DR EMBL: AF132147; AAD33594.1; -;
DR HSSP: P54725; IDV0.
DR Flybase: FBgn0026777; Rad23.
DR InterPro: IPR004806; Rad23.
DR InterPro: IPR000449; UBA.domain.
DR InterPro: IPR000626; Ubiqultin.
DR Pfam: PF00627; UBA; 2.
DR Pfam: PF00240; ubiqlutin; 1.
DR PRINTS: PR01574; TUBBYPROTEIN.
DR SMART: SM00165; UBA; 2.
DR SMART: SM00213; UBO; 1.
DR TIGRFAMs: TIGR00601; rad23; 1.
DR PROSITE: PS50053; UBIQUITIN_2; 1.
SQ SEQUENCE 414 AA; 45780 MW; 4C2E494CA116F7AB CRC64;

Query Match 23.6%; Score 481; DB 5; Length 414;
Best Local Similarity 29.3%; Pred. No. 1.8e-21;
Matches 134; Conservative 72; Mismatches 153; Indels 98; Gaps 10;

OY 1 MKNLVKTLKGNFEIEASPDASVADVKRIIEFTGQSTYRADQOMLIYQKILKDETTLE 60
DB 1 MIIITKLNQOQFTIEFAFEKTVLELKKIFERGRPE-YVAEKOKLIYAGVILTDRTVG 59
OY 61 SNGVAVENSLVIMLSKAKASSS-----GASTATTAKAPATIAQPAAPAPAPASVARTPT 114
DB 60 SYNVEKKRFIVYMLTRDSSSSNRNOLSVKESNKLITSTDSKOSMPCCEANHTNSPSTNT 119
OY 115 GAVVATETAPSPVQQAAPATVAATDADVYSGAASNLVFGNNLBOFIOOILDMGGT 174
DB 120 EDVSVLSRETRPLSSDELLIGELA-----QASIQSRASHSLMGDEYNQIVLSKVEKG--- 170
OY 175 WERTIVYRALRAAYNNPERAIDLYSGIPEVNEAOPVARAPAAQOQTNQOASPAQAPAVA 234
DB 171 YRQGVVERAMASYNPNPRAVEYLINGIP-----AEGGTFFNRLNENSTNPSL 217

OY 235 LPVQSPASAGPNNANLNFPGCVPSGSGNPGVPGAGGALDALRQLPQFQALLQVYA 294
DB 218 IIPSGPQAPASA-----TSAERSTESN-----SDPEEFKINSQPOFLQMSRLIYQ 259
OY 295 NPPILOPMIOELCKONPQILRLIOENQAEFLRVNE--SPGPGGNIIGOLAAVAPQTL 352
DB 260 NPHLLHANVIOQIQOTNPALLQILISENODAFLNMLNPIPIRESGATVPVSNARIPSTL 319
OY 353 -----TYTPPERAIOQL 365
DB 320 DWVDLSPDLEVATSAQRSAAGTSAHQSGAANDNEDLPQIGVSTRILNRQDKDAIERL 379
OY 366 EGMGFRELVLVEFACNNDDELTANYLLDHRGHEPD 402
DB 380 KALGFPEALVLQAYFACERNEBOANFL--SSSPDD 414

RESULT 14
ID O9XZE0 PRELIMINARY; PRT; 414 AA.
AC O9XZE0;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE DHR23.
GN RAD23 OR CG1836.
OS *Drosophila melanogaster* (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidae; Drosophilidae; *Drosophila*.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Nabirochkina E.N., Grischuk A.L., Soldatov A.V.;
RT "Cloning and characterization of the *Drosophila melanogaster* homologue
of the *Saccharomyces cerevisiae* gene RAD23.";
RL Genetika 35:0-0(1999)
DR EMBL: AF136606; AAD33695.1; -;
DR HSSP: P54725; IDV0.
DR Flybase: FBgn0026777; Rad23.
DR InterPro: IPR004806; Rad23.
DR InterPro: IPR000449; UBA.domain.
DR InterPro: IPR000626; Ubiqultin.
DR Pfam: PF00627; UBA; 2.
DR Pfam: PF00240; ubiqlutin; 1.
DR PRINTS: PR01574; TUBBYPROTEIN.
DR SMART: SM00165; UBA; 2.
DR SMART: SM00213; UBO; 1.
DR TIGRFAMs: TIGR00601; rad23; 1.
DR PROSITE: PS50053; UBIQUITIN_2; 1.
SQ SEQUENCE 414 AA; 45794 MW; 4C2FP94CA116F7AB CRC64;

Query Match 23.5%; Score 478; DB 5; Length 414;
Best Local Similarity 29.1%; Pred. No. 2.7e-21;
Matches 132; Conservative 72; Mismatches 154; Indels 96; Gaps 9;

OY 1 MKNLVKTLKGNFEIEASPDASVADVKRIIEFTGQSTYRADQOMLIYQKILKDETTLE 60
DB 1 MIIITKLNQOQFTIEFAFEKTVLELKKIFERGRPE-YVAEKOKLIYAGVILTDRTVG 59
OY 61 SNGVAVENSLVIMLSKAKASSS-----GASTATTAKAPATIAQPAAPAPAPASVARTPT 114
DB 60 SYNVEKKRFIVYMLTRDSSSSNRNOLSVKESNKLITSTDSKOSMPCCEANHTNSPSTNT 119
OY 115 GAVVATETAPSPVQQAAPATVAATDADVYSGAASNLVFGNNLBOFIOOILDMGGT 174
DB 120 EDVSVLSRETRPLSSDELLIGELA-----QASIQSRASHSLMGDEYNQIVLSKVEKG--- 170
OY 175 WERTIVYRALRAAYNNPERAIDLYSGIPEVNEAOPVARAPAAQOQTNQOASPAQAPAVA 234
DB 171 YRQGVVERAMASYNPNPRAVEYLINGIP-----AEGGTFFNRLNENSTNPSL 217
OY 235 LPVQSPASAGPNNANLNFPGCVPSGSGNPGVPGAGGALDALRQLPQFQALLQVYA 294

